G. SEQUENCE LISTING

5	(1)	GEN	ERAL INFORMATION
10		(i)	APPLICANT: Darrell Anderson, Nabil Hanna, John Leonard, Roland Newman and Mitchell Reff and William H. Rastetter
15		(ii)	TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL LYMPHOMA
		(iii)	NUMBER OF SEQUENCES: 8
20		(iv)	CORRESPONDING ADDRESS:
25			(A) ADDRESSEE: IDEC Pharmaceuticals Corporation (B) STREET: 11011 Torreyana Road (C) CITY: San Diego (D) STATE: California (E) COUNTRY: USA (F) ZIP: 92121
30		(v)	COMPUTER READABLE FORM:
			 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb (B) COMPUTER: Macintosh (C) OPERATING SYSTEM: MS.DOS (D) SOFTWARE: Microsoft Word 5.0
35		(vi	CURRENT APPLICATION DATA:
40			(A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
		(viii)	ATTORNEY/AGENT INFORMATION:
45			 (A) NAME: Burgoon, Richard P. Jr. (B) REGISTRATION NUMBER: 34,787 (C) REFERENCE/DOCKET NUMBER:
		(ix)	TELECOMMUNICATION INFORMATION:
50			(A) TELEPHONE: (619) 550-8500 (B) TELEFAX: (619) 550-8750

 $(\mathcal{A}_{i_1, i_2, i_3, i_4})$

5

10

(2) INFORMATION FOR SEQ ID NO: 1:

(i)	SEQUENCE	CHARACTERISTICS:
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(A) LENGTH: 8540 bases

PE: nucleic agid

ANDEDNESS: single

(D) TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic) (ii)

(iii) HYPOTHETICAL: yes

15 (iv) ANTI-SENSE: no

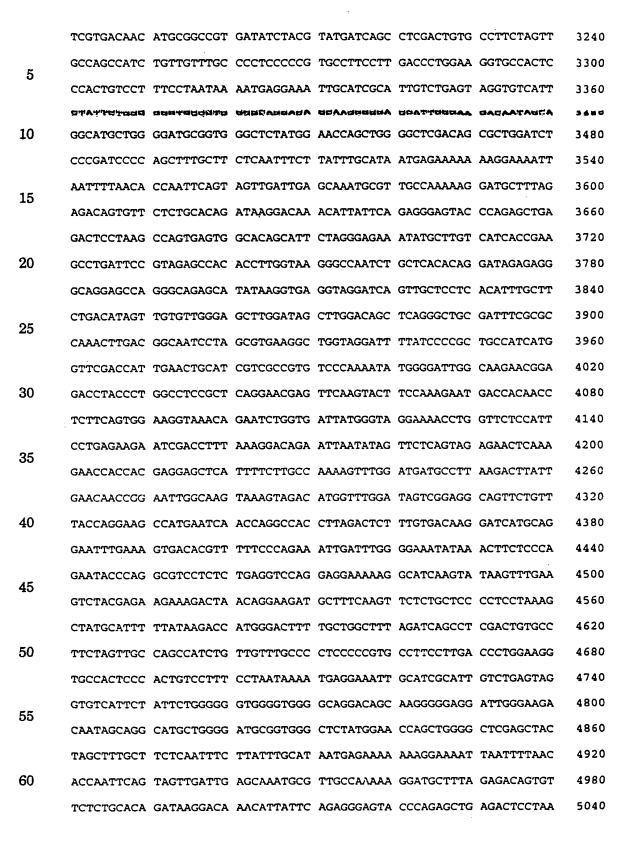
SEQUENCE DESCRIPTION: SEQ ID NO: 1: (ix)

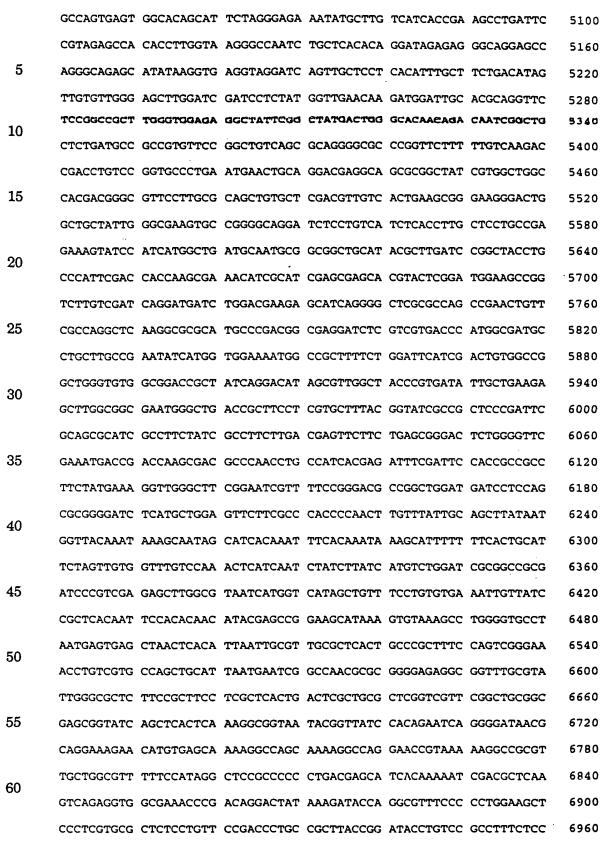




AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380 5 TGTTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC 1440 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500 GTTTGCCCCT CCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1560 10 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620 GGGGTGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680 15 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860 20 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 25 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CGCTAGCACC 2160 30 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220 GCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 2280 35 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460 40 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 2580 45 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640 2700 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 2760 50 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820 GGGCAGCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 2880 55 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940 3000 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060 60 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120 CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180









2- VI

	CTTCGGGAAG	CGTGGCGCTT	TCTCAATGCT	CACGCTGTAG	GTATCTCAGT	TCGGTGTAGG	7020
5	TCGTTCGCTC	CAAGCTGGGC	TGTGTGCACG	AACCCCCCGT	TCAGCCCGAC	CGCTGCGCCT	7080
	TATCCGGTAA	CTATCGTCTT	GAGTCCAACC	CGGTAAGACA	CGACTTATCG	CCACTGGCAG	7140
	CACCACTOG	TAACAGGATT	AGCAGAGCGA	COTATOTAGO	саотостаса	CACTTCTTCA	7200
10	AGTGGTGGCC	TAACTACGGC	TACACTAGAA	GGACAGTATT	TGGTATCTGC	GCTCTGCTGA	7260
	AGCCAGTTAC	CTTCGGAAAA	AGAGTTGGTA	GCTCTTGATC	CGGCAAACAA	ACCACCGCTG	7320
15	GTAGCGGTGG	TTTTTTTGTT	TGCAAGCAGC	AGATTACGCG	CAGAAAAAA	GGATCTCAAG	7380
10	AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAAC	TCACGTTAAG	7440
	GGATTTTGGT	CATGAGATTA	TCAAAAAGGA	TCTTCACCTA	GATCCTTTTA	AATTAAAAAT	7500
20	GAAGTTTTAA	ATCAATCTAA	AGTATATAŢG	AGTAAACTTG	GTCTGACAGT	TACCAATGCT	7560
	TAATCAGTGA	GGCACCTATC	TCAGCGATCT	GTCTATTTCG	TTCATCCATA	GTTGCCTGAC	7620
25	TCCCCGTCGT	GTAGATAACT	ACGATACGGG	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	7680
20	TGATACCGCG	AGACCCACGC	TCACCGGCTC	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	7740
	GAAGGCCGA	GCGCAGAAGT	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	7800
30	GTTGCCGGGA	AGCTAGAGTA	AGTAGTTCGC	CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	7860
	TTGCTACAGG	CATCGTGGTG	TCACGCTCGT	CGTTTGGTAT	GGCTTCATTC	AGCTCCGGTT	7920
35	CCCAACGATC	AAGGCGAGTT	ACATGATCCC	CCATGTTGTG	CAAAAAAGCG	GTTAGCTCCT	7980
00	TCGGTCCTCC	GATCGTTGTC	AGAAGTAAGT	TGGCCGCAGT	GTTATCACTC	ATGGTTATGG	8040
	CAGCACTGCA	TAATTCTCTT	ACTGTCATGC	CATCCGTAAG	ATGCTTTTCT	GTGACTGGTG	8100
40	AGTACTCAAC	CAAGTCATTC	TGAGAATAGT	GTATGCGGCG	ACCGAGTTGC	TCTTGCCCGG	8160
	CGTCAATACG	GGATAATACC	GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTGGAA	8220
45	AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	8280
4 0	AACCCACTCG	TGCACCCAAC	TGATCTTCAG	CATCTTTTAC	TTTCACCAGC	GTTTCTGGGT	8340
	GAGCAAAAAC	AGGAAGGCAA	AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	8400
50	GAATACTCAT	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	8460
•	TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAAACA	AATAGGGGTT	CCGCGCACAT	8520
55	TTCCCCGAAA	AGTGCCACCT					8540

INFORMATION FOR SEQ ID NO: 2: (3)

SEQUENCE CHARACTERISTICS: 60 (i)

(A) LENGTH: 9209 bases

60

5	(ii)	MOLECULE	TYPE: DN	IA (genomic)									
	(iii)	нұротнет	ICAL: yes											
	(iv) ANTI-SENSE: no													
10	(ix)	SEQUENCE	DESCRIPT	TION: SEQ	ID NO: 2:									
15	GACGTCGCGG	CCGCTCTAGG	CCTCCAAAAA	AGCCTCCTCA	CTACTTCTGG	AATAGCTCAG	60							
10	AGGCCGAGGC	GGCCTCGGCC	TCTGCATAAA	TAAAAAAAAT	TAGTCAGCCA	TGCATGGGGC	120							
	GGAGAATGGG	CGGAACTGGG	CGGAGTTAGG	GGCGGGATGG	GCGGAGTTAG	GGGCGGGACT	180							
20	ATGGTTGCTG	ACTAATTGAG	ATGCATGCTT	TGCATACTTC	TGCCTGCTGG	GGAGCCTGGG	240							
	GACTTTCCAC	ACCTGGTTGC	TGACTAATTG	AGATGCATGC	TTTGCATACT	TCTGCCTGCT	300							
25	GGGGAGCCTG	GGGACTTTCC	ACACCCTAAC	TGACACACAT	TCCACAGAAT	TAATTCCCCT	360							
4 0	AGTTATTAAT	AGTAATCAAT	TACGGGGTCA	TTAGTTCATA	GCCCATATAT	GGAGTTCCGC	420							
	GTTACATAAC	TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC	CCAACGACCC	CCGCCCATTG	480							
30	ACGTCAATAA	TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	540							
	TGGGTGGACT	ATTTACGGTA	AACTGCCCAC	TTGGCAGTAC	ATCAAGTGTA	TCATATGCCA	600							
35	AGTACGCCCC	CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATTA	TGCCCAGTAC	660							
39	ATGACCTTAT	GGGACTTTCC	TACTTGGCAG	TACATCTACG	TATTAGTCAT	CGCTATTACC	720							
	ATGGTGATGC	GGTTTTGGCA	GTACATCAAT	GGGCGTGGAT	AGCGGTTTGA	CTCACGGGGA	780							
40	TTTCCAAGTC	TCCACCCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	840							
	GACTTTCCAA	AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG	TAGGCGTGTA	900							
	CGGTGGGAGG	TCTATATAAG	CAGAGCTGGG	TACGTGAACC	GTCAGATCGC	CTGGAGACGC	960							
45	CATCACAGAT	CTCTCACTAT	GGATTTTCAG	GTGCAGATTA	TCAGCTTCCT	GCTAATCAGT	1020							
	GCTTCAGTCA	TAATGTCCAG	AGGACAAATT	GTTCTCTCCC	AGTCTCCAGC	AATCCTGTCT	1080							
50	GCATCTCCAG	GGGAGAAGGT	CACAATGACT	TGCAGGGCCA	GCTCAAGTGT	AAGTTACATC	1140							
	CACTGGTTCC	AGCAGAAGCC	AGGATCCTCC	CCCAAACCCT	GGATTTATGC	CACATCCAAC	1200							
	CTGGCTTCTG	GAGTCCCTGT	TCGCTTCAGT	GGCAGTGGGT	CTGGGACTTC	TTACTCTCTC	1260							
55	ACAATCAGCA	GAGTGGAGGC	TGAAGATGCT	GCCACTTATT	ACTGCCAGCA	GTGGACTAGT	1320							

1380

1440

(B)

(C) (D)

TYPE: nucleic acid

STRANDEDNESS: single TOPOLOGY: circular

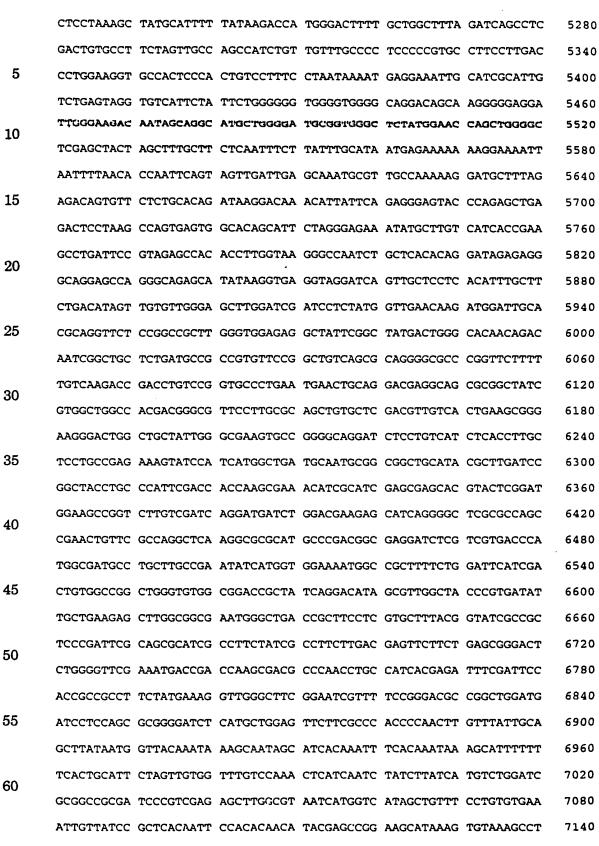


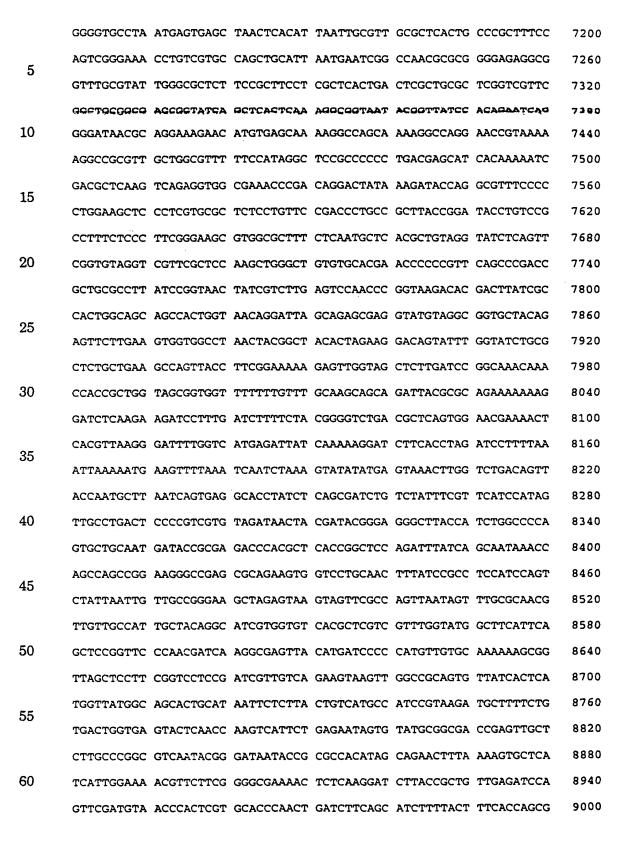
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	TGCCTGCTGA	ATAACTTCTA	TCCCAGAGAG	GCCAAAGTAC	AGTGGAAGGT	GGATAACGCC	1500
	CTCCAATCGG	GTAACTCCCA	GGAGAGTGTC	ACAGAGCAGG	ACAGCAAGGA	CAGCACCTAC	1560
5	AGCCTCAGCA	GCACCCTGAC	GCTGAGCAAA	GCAGACTACG	AGAAACACAA	AGTCTACGCC	1620
	TGCGAAGTCA	CCCATCAGGG	CCTGAGCTCG	CCCGTCACAA	AGAGCTTCAA	CAGGGGAGAG	1680
10	TGTTGAATTC	AGATCCGTTA	ACGGTTACCA	ACTACCTAGA	CTGGATTCGT	GACAACATGC	1740
10	GGCCGTGATA	TCTACGTATG	ATCAGCCTCG	ACTGTGCCTT	CTAGTTGCCA	GCCATCTGTT	1800
	GTTTGCCCCT	CCCCCGTGCC	TTCCTTGACC	CTGGAAGGTG	CCACTCCCAC	TGTCCTTTCC	1860
15	TAATAAAATG	AGGAAATTGC	ATCGCATTGT	CTGAGTAGGT	GTCATTCTAT	TCTGGGGGGT	1920
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00	GCGGTGGGCT	CTATGGAACC	AGCTGGGGCT	CGACAGCTAT	GCCAAGTACG	CCCCCTATTG	2040
20	ACGTCAATGA	CGGTAAATGG	CCCGCCTGGC	ATTATGCCCA	GTACATGACC	TTATGGGACT	2100
	TTCCTACTTG	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG	ATGCGGTTTT	2160
25	GGCAGTACAT	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCCA	AGTCTCCACC	2220
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00	GTAACAACTC	CGCCCCATTG	ACGCAAATGG	GCGGTAGGCG	TGTACGGTGG	GAGGTCTATA	2340
30	TAAGCAGAGC	TGGGTACGTC	CTCACATTCA	GTGATCAGCA	CTGAACACAG	ACCCGTCGAC	2400
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35	GTACAACTGC	AGCAGCCTGG	GGCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATGTCC	2520
	TGCAAGGCTT	CTGGCTACAC	ATTTACCAGT	TACAATATGC	ACTGGGTAAA	ACAGACACCT	2580
40	GGTCGGGGCC	TGGAATGGAT	TGGAGCTATT	TATCCCGGAA	ATGGTGATAC	TTCCTACAAT	2640
40	CAGAAGTTCA	AAGGCAAGGC	CACATTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	2700
	CAGCTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTATT	ACTGTGCAAG	ATCGACTTAC	2760
45	TACGGCGGTG	ACTGGTACTT	CAATGTCTGG	GGCGCAGGGA	CCACGGTCAC	CGTCTCTGCA	2820
	GCTAGCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCCT	CCTCCAAGAG	CACCTCTGGG	2880
	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTCG	2940
50	TGGAACTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCI	ACAGTCCTCA	3000
	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	3060
55	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	: AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120
						CCTGGGGGGA	3180
						CCGGACCCCT	3240
60						GTTCAACTGG	3300
						GCAGTACAAC	3360

AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480 5 AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC CCGGGATGAG 3540 CTGACGAGA ACCAGTGAG CCTGACCTGC CTGGTGAAAG GCTTCTATCC GAGGACATG 3600 10 GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT ACAAGACCAC GCCTCCCGTG 3660 CTGGACTCCG ACGCTCCTT CTTCCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780 15 CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA TGAGGATCCG TTAACGGTTA CCAACTACCT 3840 AGACTGGATT CGTGACAACA TGCGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900 20 CTTCTAGTTG CCAGCCATCT GTTGTTTGCC CCTCCCCGT GCCTTCCTTG ACCCTGGAAG 3960 GTGCCACTCC CACTGTCCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020 GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080 25 ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140 4200 GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTTCTT ATTTGCATAA TGAGAAAAAA 30 AGGAAAATTA ATTTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260 ATGCTTTAGA GACAGTGTTC TCTGCACAGA TAAGGACAAA CATTATTCAG AGGGAGTACC 4320 CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTC TAGGGAGAAA TATGCTTGTC 4380 35 ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCCAATCTG CTCACACAGG 4440 ATAGAGAGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500 40 CATTTGCTTC TGACATAGTT GTGTTGGGAG CTTGGATAGC TTGGACAGCT CAGGGCTGCG 4560 ATTTCGCGCC AAACTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620 GCCATCATGG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680 45 AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740 ACCACAACCT CTTCAGTGGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800 50 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA TGATGCCTTA 4920 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980 55 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCCAGAAA TTGATTTGGG GAAATATAAA 5100 60 CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220





	TTT	CTGGGT	G AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC	9060
	GGA	AATGTT	G AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT	9120
5	ATT	GTCTCA	T GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC	9180
	CGC	GCACAT	T TCCCCGAAAA GTGCCACCT	9209
10	(4)	INFO	RMATION FOR SEQ ID NO: 3:	
		(i)	SEQUENCE CHARACTERISTICS:	
15			 (A) LENGTH: 54 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20		(ii)	MOLECULE TYPE: DNA (genomic)	
20		(iii)	HYPOTHETICAL: yes	
		(iv)	ANTI-SENSE: no	
25		(ix)	SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
			C ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT	52 2
30	(5)	INFO	RMATION FOR SEQ ID NO: 4:	
		(i)	SEQUENCE CHARACTERISTICS:	
35			 (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
40		(ii)	MOLECULE TYPE: DNA (genomic)	
		(iii)	HYPOTHETICAL: yes	
45		(iv)	ANTI-SENSE: yes	
		(ix)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
50		5' TG	C AGC ATC CGT ACG TTT GAT TTC CAG CTT 3'	30
	(6)	INFO	RMATION FOR SEQ ID NO: 5:	
==		(i)	SEQUENCE CHARACTERISTICS:	
-				

-			((A) 3) C) O)	TYI	PE:	nucle DED	eic a NES : lir	cid SS: s		e							
5		(ii) MOLECULE TYPE: DNA (genomic)																
		(ili)	(iii) HYPOTHETICAL: yes															
10		(iv)	Α	NTI	SEN	NSE:	no											
		(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5:																
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	АТА	ATG	TCC	AGA	GGG	CAA	ATT	GTT	CTC	TCC	CAG	TCT	CCA	GCA	ATC	CTG	TCT	102
20	GCA	TCT	CCA	GGG	GAG	AAG	GTC	ACA	ATG	ACT	TGC	AGG	GCC	AGC	TCA	AGT	GTA	153
20	AGT	TAC	ATC	CAC	TGG	TTC	CAG	CAG	AAG	CCA	GGA	TCC	TCC	CCC	AAA	CCC	TGG	204
	ATT	TAT	GCC	ACA	TCC	AAC	CTG	GCT	TCT	GGA	GTC	CCT	GTT	CGC	TTC	AGT	GGC	255
25	AGT	GGG	TCT	GGG	ACT	TCT	TAC	TCT	CTC	ACA	ATC	AGC	AGA	GTG	GAG	GCT	GAA	306
	GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAG	CAG	TGG	ACT	AGT	AAC	CCA	CCC	ACG	TTC	357
30	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATC	AAA									384
	(7)	INF	ORI	MAT	ION	FOI	R SE	Q II	NC	: 6:								
		(i) SEQUENCE CHARACTERISTICS:																
35			(E	A) 3) C) O)	TYI	PE: RAN	nucle DED	27 ba eic a NES	cid SS: s	singl	e							
40		(ii)	·					E: D		gene	omic)						
		(iii)	H	YPO	TH	ETIC	CAL:	yes										
45		(iv)	A	NTI	-SEN	NSE:	no											
		(ix)	S	EQU	JEN(CE I	DESC	CRIF	OIT	N: \$	SEQ	ID N	10:	6:				
50		5' (GCG (GCT (ccc i	ACG (CGT (GTC (CTG '	rcc (CAG	3 '						27

	(8)	IN	FOF	RMA'	TIOI	V FC	R S	EQ I	D N	O: 7	' :							
		(i)	1	SEQ	UEN	ICE	CHA	\RA(CTE	RIST	rics	:						
5			((A) LENGTH: 29 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear														
10		(ii)]	MOL	ECU	JLE	TYF	PE: 1	DNA	(ger	nomi	c)						
		(iii)]	HYP	IYPOTHETICAL: yes													
		(iv)	ANT	I-SE	NSE	Σ: y ε	s										
15		(ix) :	SEQ	UEN	CE	DES	CRI	PTI(ON:	SEG	QI Ş	NO:	7:				
		5'	GGS	TGT	TGT	GCT	AGC	TGM	RGA	GAC	RGT	GA :	3 '	29				
20	(9)	TNT	ror	ን አ ፈ ላ ላ	יוח איז	ለ ፔ ር	ים פי	eo t	D N	∩.	•							
	(9)							•										
		(i)		_					CTEI		COI	•						
25			 (A) LENGTH: 420 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 															
30		(ii)	1	MOL	ECU	ЛLE	TYF	E: I	DNA	(ger	nomi	c)						
		(iii)]	HYP	OTH	ETI	CAL	.: ye	s									
0.5		(iv) .	ANT	I-SE	NSE	E: no)										
35		(ix) :	SEQ	UEN	ICE	DES	CRI	PTI(ON:	SEG	(ID	NO:	8:				
40	ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	GTC	51
40	CTG	TCC	CAG	GTA	CAA	CTG	CAG	CAG	CCT	GGG	GCT	GAG	CTG	GTG	AAG	ССТ	GGG	102
	GCC	TCA	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTT	ACC	AGT	TAC	153
45	AAT	ATG	CAC	TGG	GTA	AAA	CAG	ACA	CCT	GGT	CGG	GGC	CTG	GAA	TGG	ATT	GGA	204
	GCT	TTA	TAT	CCC	GGA	AAT	GGT	GAT	ACT	TCC	TAC	AAT	CAG	AAG	TTC	AAA	GGC	255
50	AAG	GCC	ACA	TTG	ACT	GCA	GAC	AAA	TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG	CTC	305
	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCG	GTC	TAT	TAC	TGT	GCA	AGA	TCG	ACT	357
	TAC	TAC	GGC	GGT	GAC	TGG	TAC	TTC	AAT	GTC	TGG	GGC	GCA	GGG	ACC	ACG	GTC	408